



# *Ppargc1a* Cas9-KO Strategy

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**Reviewer:**

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**2019-9-28**

# Project Overview

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**Project Name*****Ppargc1a***

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**Project type****Cas9-KO**

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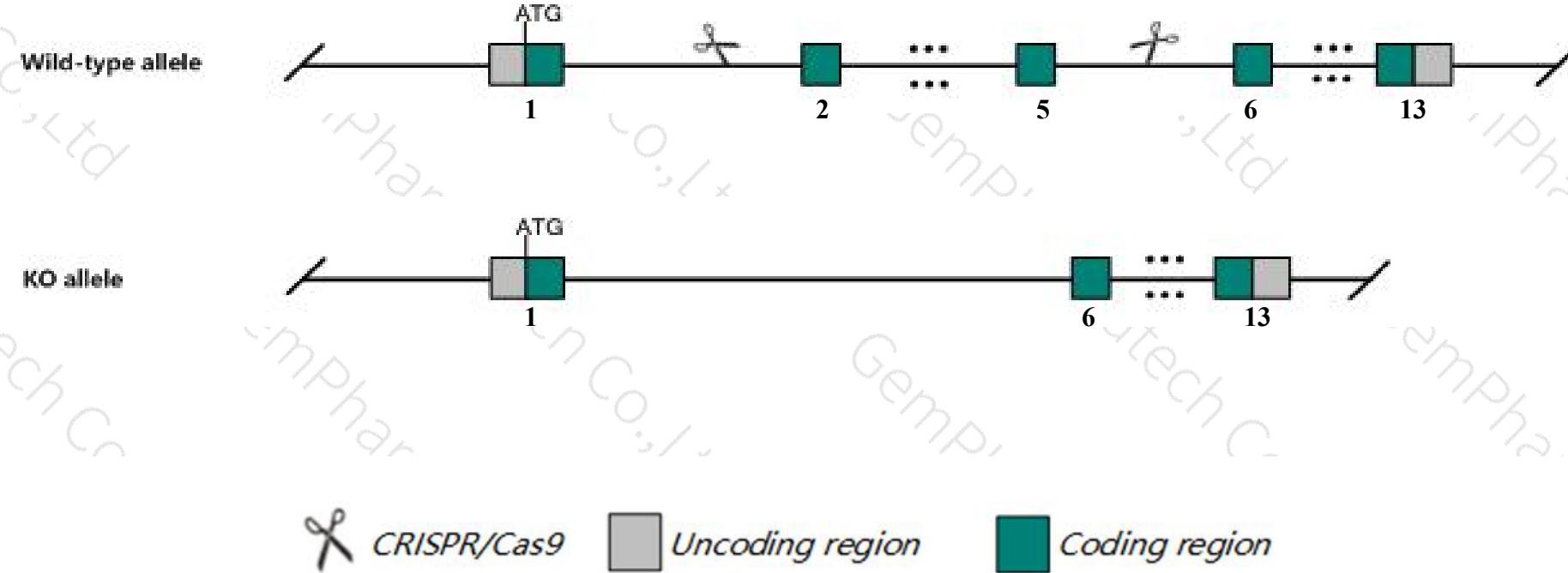
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**Strain background****C57BL/6JGpt**

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# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ppargc1a* gene. The schematic diagram is as follows:



# Technical routes

- The *Ppargc1a* gene has 5 transcripts. According to the structure of *Ppargc1a* gene, exon2-exon5 of *Ppargc1a-203* (ENSMUST00000132734.7) transcript is recommended as the knockout region. The region contains 706bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ppargc1a* gene. The brief process is as follows: CRISPR/Cas9 sys



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# Notice

- According to the existing MGI data, Homozygous null mice display partial postnatal lethality, abnormal glucose and insulin homeostasis, resistance to diet induced obesity, increased oxygen consumption, spongiform encephalopathy, hyperactivity, increased startle reflex, and limb grasping.
- The *Ppargc1a* gene is located on the Chr5. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

# Gene information (NCBI)



## Ppargc1a peroxisome proliferative activated receptor, gamma, coactivator 1 alpha [Mus musculus (house mouse)]

Gene ID: 19017, updated on 9-Apr-2019

### Summary



**Official Symbol** Ppargc1a provided by [MGI](#)

**Official Full Name** peroxisome proliferative activated receptor, gamma, coactivator 1 alpha provided by [MGI](#)

**Primary source** [MGI:MGI:1342774](#)

**See related** [Ensembl:ENSMUSG00000029167](#)

**Gene type** protein coding

**RefSeq status** REVIEWED

**Organism** [Mus musculus](#)

**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

**Also known as** A830037N07Rik, Gm11133, PGC-1, PPARGC-1-alpha, Pgc-1alpha, Pgc1, Pgco1, Ppargc1

**Summary** This gene encodes a transcriptional coactivator that induces and coordinates gene expression regulating mitochondrial biogenesis, respiration, hepatic gluconeogenesis, thermogenic program in brown fat and muscle fiber-type switching. Mice lacking the encoded protein exhibit reduced thermogenic capacity, hyperactivity and resistance to diet-induced obesity. Mice lacking the encoded protein specifically in the heart exhibit peripartum cardiomyopathy. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Sep 2015]

**Expression** Broad expression in heart adult (RPKM 4.1), frontal lobe adult (RPKM 3.9) and 22 other tissues [See more](#)

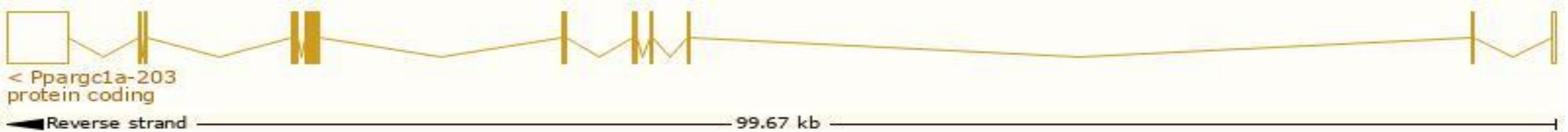
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

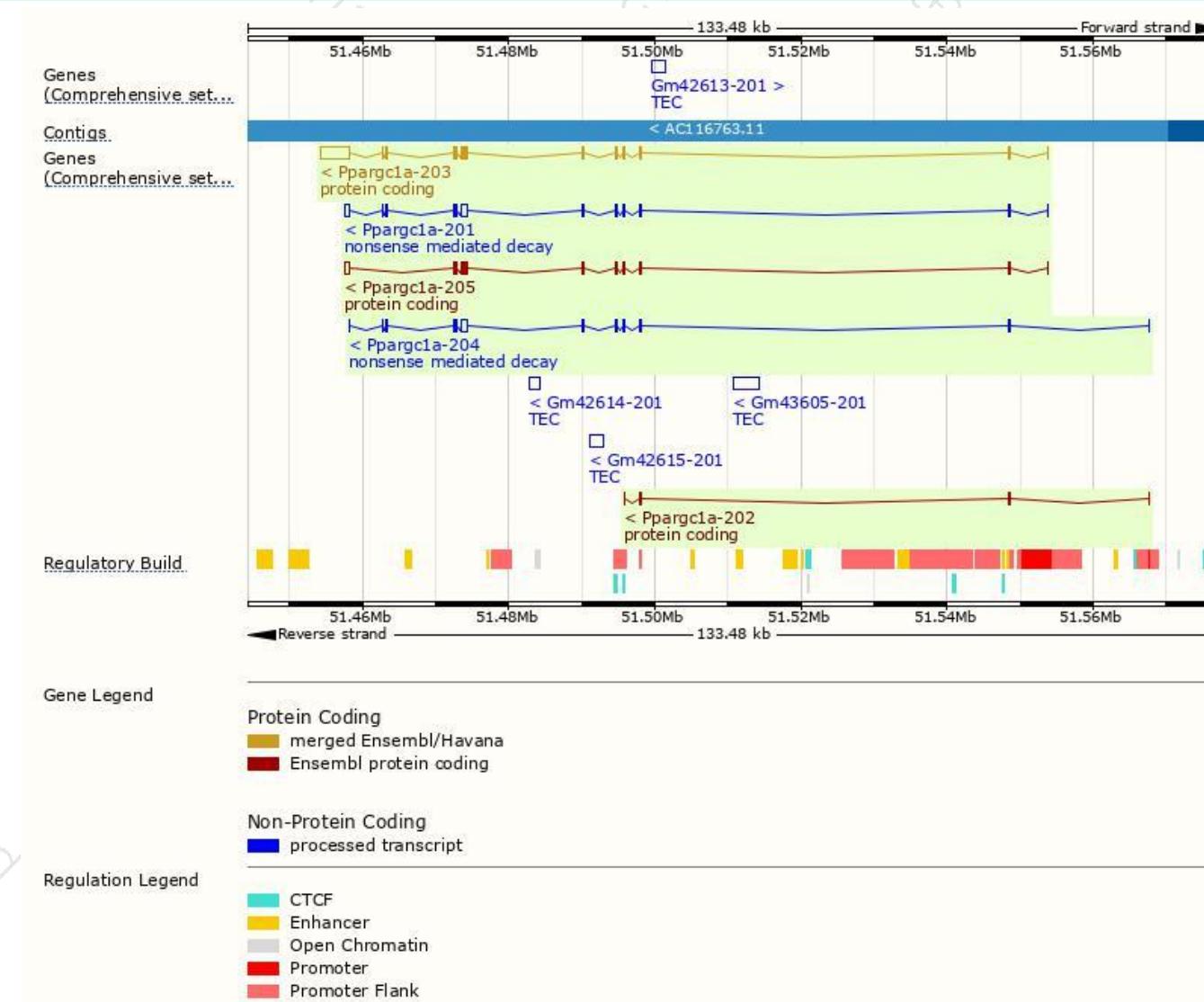
The gene has 5 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ppargc1a-203	<a href="#">ENSMUST00000132734.7</a>	6464	<a href="#">797aa</a>	Protein coding	<a href="#">CCDS19282</a>	<a href="#">O70343</a>	TSL:1 GENCODE basic APPRIS P1
Ppargc1a-205	<a href="#">ENSMUST00000196968.4</a>	2754	<a href="#">696aa</a>	Protein coding	-	<a href="#">A0A0G2JGG3</a>	TSL:5 GENCODE basic
Ppargc1a-202	<a href="#">ENSMUST00000127135.2</a>	488	<a href="#">142aa</a>	Protein coding	-	<a href="#">D3YZS8</a>	CDS 3' incomplete TSL:5
Ppargc1a-201	<a href="#">ENSMUST00000031059.13</a>	3041	<a href="#">270aa</a>	Nonsense mediated decay	-	<a href="#">Q3LIG2</a>	TSL:1
Ppargc1a-204	<a href="#">ENSMUST00000151104.7</a>	2452	<a href="#">266aa</a>	Nonsense mediated decay	-	<a href="#">O70343</a>	TSL:1

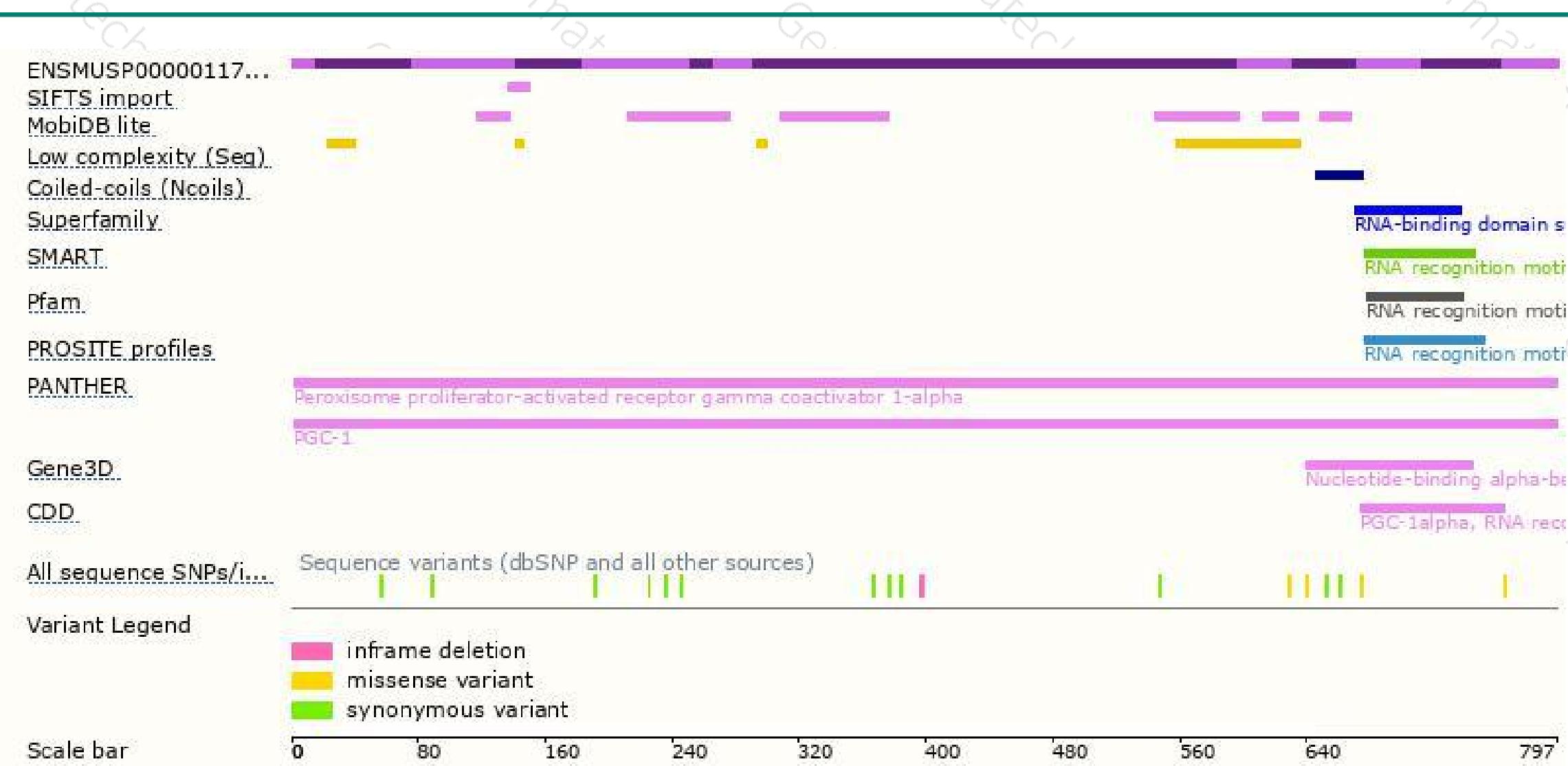
The strategy is based on the design of *Ppargc1a-203* transcript, The transcription is shown below



# Genomic location distribution



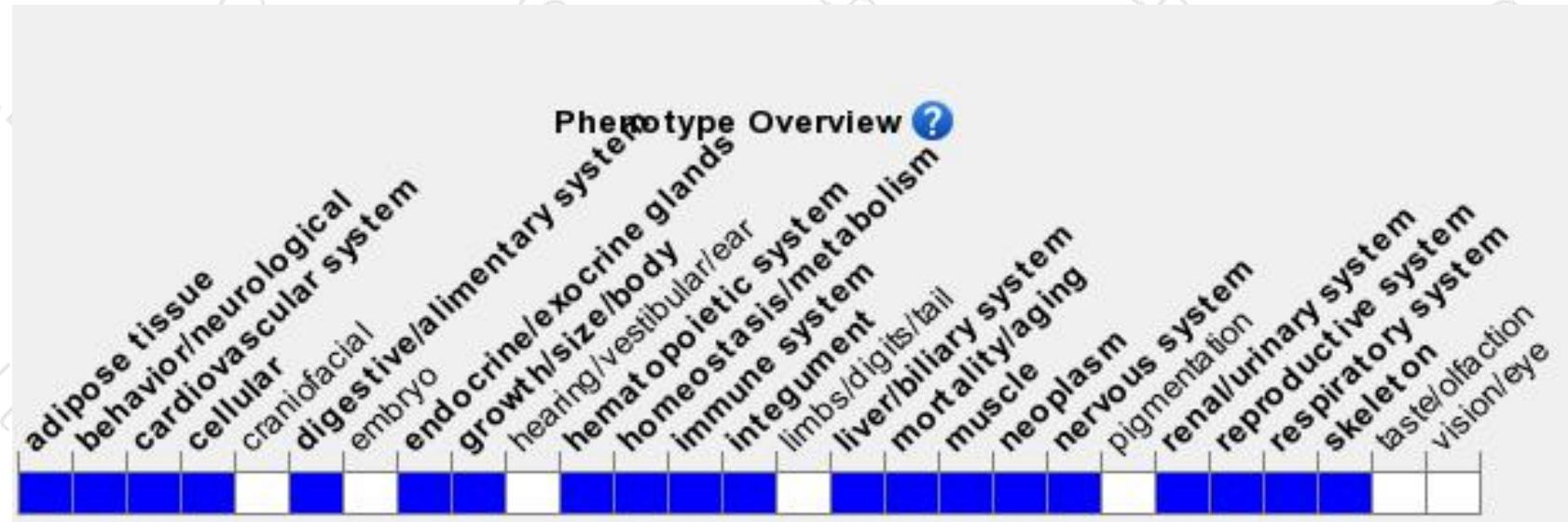
# Protein domain





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# Mouse phenotype description(MGI )



*Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).*

According to the existing MGI data, Homozygous null mice display partial postnatal lethality, abnormal glucose and insulin homeostasis, resistance to diet induced obesity, increased oxygen consumption, spongiform encephalopathy, hyperactivity, increased startle reflex, and limb grasping.



If you have any questions, you are welcome to inquire.

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